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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=7; day=28; hr=13; min=50; sec=5; ms=426; ]

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Application No: 10718986 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2008-07-25 21:55:54.597  
**Finished:** 2008-07-25 21:55:55.587  
**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 990 ms  
**Total Warnings:** 1  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 12  
**Actual SeqID Count:** 12

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (10)

SEQUENCE LISTING

<110> Yu, Mang  
Fang, Fang

<120> Broad Spectrum Anti-Viral Therapeutics  
And Prophylaxis

<130> 21865-002001/6502

<140> 10718986  
<141> 2003-11-21

<150> US 60/428,535  
<151> 2002-11-12

<150> US 60/464,217  
<151> 2003-04-19

<160> 12

<170> FastSEQ for Windows Version 4.0

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<211> 58  
<212> PRT  
<213> Bos taurus

<400> 1  
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1 5 10 15  
Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr  
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Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys Ser Ala  
35 40 45  
Glu Asp Cys Met Arg Thr Cys Gly Gly Ala  
50 55

<210> 2  
<211> 24  
<212> PRT  
<213> Homo sapiens

<400> 2  
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1 5 10 15  
Ile Ile Lys Lys Leu Leu Glu Ser  
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<210> 3  
<211> 27  
<212> PRT  
<213> Homo sapiens

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Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val  
1 5 10 15  
Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser  
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<210> 4  
<211> 34  
<212> PRT  
<213> Homo sapiens

<400> 4  
Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys  
1 5 10 15  
Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp  
20 25 30  
Lys Ser

<210> 5  
<211> 34  
<212> PRT  
<213> Homo sapiens

<400> 5  
Glu Leu Arg Val Arg Leu Ala Ser His Leu Arg Lys Leu Arg Lys Arg  
1 5 10 15  
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20 25 30  
Ala Gly

<210> 6  
<211> 12  
<212> PRT  
<213> Homo sapiens

<400> 6  
Arg Arg Leu Arg Arg Met Glu Ser Glu Ser Glu Ser  
1 5 10

<210> 7  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 7  
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Lys Lys Lys Asn Pro  
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<210> 8  
<211> 379  
<212> PRT  
<213> Homo sapiens

<400> 8

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Ser Leu Leu Ala Phe Ala Glu Gln Arg Ala Ser Lys Lys Asp Glu His  
35 40 45  
Ala Glu Leu Ile Val Leu Arg Arg Gly Asp Tyr Asp Ala Pro Thr His  
50 55 60  
Gln Val Gln Trp Gln Ala Gln Glu Val Val Ala Gln Ala Arg Leu Asp  
65 70 75 80  
Gly His Arg Ser Met Asn Pro Cys Pro Leu Tyr Asp Ala Gln Thr Gly  
85 90 95  
Thr Leu Phe Leu Phe Phe Ile Ala Ile Pro Gly Gln Val Thr Glu Gln  
100 105 110  
Gln Gln Leu Gln Thr Arg Ala Asn Val Thr Arg Leu Cys Gln Val Thr  
115 120 125  
Ser Thr Asp His Gly Arg Thr Trp Ser Ser Pro Arg Asp Leu Thr Asp  
130 135 140  
Ala Ala Ile Gly Pro Ala Tyr Arg Glu Trp Ser Thr Phe Ala Val Gly  
145 150 155 160  
Pro Gly His Cys Leu Gln Leu Asn Asp Arg Ala Arg Ser Leu Val Val  
165 170 175  
Pro Ala Tyr Ala Tyr Arg Lys Leu His Pro Ile Gln Arg Pro Ile Pro  
180 185 190  
Ser Ala Phe Cys Phe Leu Ser His Asp His Gly Arg Thr Trp Ala Arg  
195 200 205  
Gly His Phe Val Ala Gln Asp Thr Leu Glu Cys Gln Val Ala Glu Val  
210 215 220  
Glu Thr Gly Glu Gln Arg Val Val Thr Leu Asn Ala Arg Ser His Leu  
225 230 235 240  
Arg Ala Arg Val Gln Ala Gln Ser Thr Asn Asp Gly Leu Asp Phe Gln  
245 250 255  
Glu Ser Gln Leu Val Lys Lys Leu Val Glu Pro Pro Pro Gln Gly Cys  
260 265 270  
Gln Gly Ser Val Ile Ser Phe Pro Ser Pro Arg Ser Gly Pro Gly Ser  
275 280 285  
Pro Gln Trp Leu Leu Tyr Thr His Pro Thr His Ser Trp Gln Arg Ala  
290 295 300  
Asp Leu Gly Ala Tyr Leu Asn Pro Arg Pro Pro Ala Pro Glu Ala Trp  
305 310 315 320  
Ser Glu Pro Val Leu Leu Ala Lys Gly Ser Cys Ala Tyr Ser Asp Leu  
325 330 335  
Gln Ser Met Gly Thr Gly Pro Asp Gly Ser Pro Leu Phe Gly Cys Leu  
340 345 350  
Tyr Glu Ala Asn Asp Tyr Glu Glu Ile Val Phe Leu Met Phe Thr Leu  
355 360 365  
Lys Gln Ala Phe Pro Ala Glu Tyr Leu Pro Gln  
370 375

<210> 9  
<211> 424  
<212> PRT  
<213> Homo sapiens

<400> 9  
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20 25 30  
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35 40 45  
Thr Pro Glu Ala Val Gln Ile Ala Thr Gly Arg Asn Ala Ala Arg Leu  
50 55 60  
Cys Cys Val Ala Ser Arg Asp Ala Gly Leu Ser Trp Gly Ser Ala Arg  
65 70 75 80  
Asp Leu Thr Glu Glu Ala Ile Gly Gly Ala Val Gln Asp Trp Ala Thr  
85 90 95  
Phe Ala Val Gly Pro Gly His Gly Val Gln Leu Pro Ser Gly Arg Leu  
100 105 110  
Leu Val Pro Ala Tyr Thr Tyr Arg Val Asp Arg Leu Glu Cys Phe Gly  
115 120 125  
Lys Ile Cys Arg Thr Ser Pro His Ser Phe Ala Phe Tyr Ser Asp Asp  
130 135 140  
His Gly Arg Thr Trp Arg Cys Gly Gly Leu Val Pro Asn Leu Arg Ser  
145 150 155 160  
Gly Glu Cys Gln Leu Ala Ala Val Asp Gly Gly Gln Ala Gly Ser Phe  
165 170 175  
Leu Tyr Cys Asn Ala Arg Ser Pro Leu Gly Ser Arg Val Gln Ala Leu  
180 185 190  
Ser Thr Asp Glu Gly Thr Ser Phe Leu Pro Ala Glu Arg Val Ala Ser  
195 200 205  
Leu Pro Glu Thr Ala Trp Gly Cys Gln Gly Ser Ile Val Gly Phe Pro  
210 215 220  
Ala Pro Ala Pro Asn Arg Pro Arg Asp Asp Ser Trp Ser Val Gly Pro  
225 230 235 240  
Arg Ser Pro Leu Gln Pro Pro Leu Leu Gly Pro Gly Val His Glu Pro  
245 250 255  
Pro Glu Glu Ala Ala Val Asp Pro Arg Gly Gly Gln Val Pro Gly Gly  
260 265 270  
Pro Phe Ser Arg Leu Gln Pro Arg Gly Asp Gly Pro Arg Gln Pro Gly  
275 280 285  
Pro Arg Pro Gly Val Ser Gly Asp Val Gly Ser Trp Thr Leu Ala Leu  
290 295 300  
Pro Met Pro Phe Ala Ala Pro Pro Gln Ser Pro Thr Trp Leu Leu Tyr  
305 310 315 320  
Ser His Pro Val Gly Arg Arg Ala Arg Leu His Met Gly Ile Arg Leu  
325 330 335  
Ser Gln Ser Pro Leu Asp Pro Arg Ser Trp Thr Glu Pro Trp Val Ile  
340 345 350  
Tyr Glu Gly Pro Ser Gly Tyr Ser Asp Leu Ala Ser Ile Gly Pro Ala  
355 360 365  
Pro Glu Gly Gly Leu Val Phe Ala Cys Leu Tyr Glu Ser Gly Ala Arg  
370 375 380  
Thr Ser Tyr Asp Glu Ile Ser Phe Cys Thr Phe Ser Leu Arg Glu Val  
385 390 395 400  
Leu Glu Asn Val Pro Ala Ser Pro Lys Pro Pro Asn Leu Gly Asp Lys

405 Pro Arg Gly Cys Cys Trp Pro Ser  
420

410

415

<210> 10  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic construct

<400> 10  
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1 5

<210> 11  
<211> 2742  
<212> DNA  
<213> Actinomyces viscosus

<220>  
<223> nanH gene for sialidase

<400> 11  
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ggcctggccg acgtcaccat cacgcaggtg aacgcgcccgc cggacggcct ctactccgtc 180  
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gacggcacca tggcgccagcc gaccgggtcg ccagcgcgccc gagtgcgcg cggacgcagg 2580  
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aacacgcgac gagccggtaa tccggctctg agcactgact ga 2742

<210> 12

<211> 913

<212> PRT

<213> *Actinomyces viscosus*

<220>

<223> nanH sialidase

<400> 12

Met Thr Ser His Ser Pro Phe Ser Arg Arg Arg Leu Pro Ala Leu Leu

1 5 10 15

Gly Ser Leu Pro Leu Ala Ala Thr Gly Leu Ile Ala Ala Ala Pro Pro

20 25 30

Ala His Ala Val Pro Thr Ser Asp Gly Leu Ala Asp Val Thr Ile Thr

35 40 45

Gln Val Asn Ala Pro Ala Asp Gly Leu Tyr Ser Val Gly Asp Val Met

50 55 60

Thr Phe Asn Ile Thr Leu Thr Asn Thr Ser Gly Glu Ala His Ser Tyr

65 70 75 80

Ala Pro Ala Ser Thr Asn Leu Ser Gly Asn Val Ser Lys Cys Arg Trp

85 90 95

Arg Asn Val Pro Ala Gly Thr Thr Lys Thr Asp Cys Thr Gly Leu Ala

100 105 110

Thr His Thr Val Thr Ala Glu Asp Leu Lys Ala Gly Gly Phe Thr Pro

115 120 125

Gln Ile Ala Tyr Glu Val Lys Ala Val Glu Tyr Ala Gly Lys Ala Leu

130 135 140

Ser Thr Pro Glu Thr Ile Lys Gly Ala Thr Ser Pro Val Lys Ala Asn

145 150 155 160

Ser Leu Arg Val Glu Ser Ile Thr Pro Ser Ser Ser Gln Glu Asn Tyr

165 170 175

Lys Leu Gly Asp Thr Val Ser Tyr Thr Val Arg Val Arg Ser Val Ser

180 185 190

Asp Lys Thr Ile Asn Val Ala Ala Thr Glu Ser Ser Phe Asp Asp Leu

195 200 205

Gly Arg Gln Cys His Trp Gly Gly Leu Lys Pro Gly Lys Gly Ala Val

210 215 220

Tyr Asn Cys Lys Pro Leu Thr His Thr Ile Thr Gln Ala Asp Val Asp

225 230 235 240

Ala Gly Arg Trp Thr Pro Ser Ile Thr Leu Thr Ala Thr Gly Thr Asp

245	250	255
Gly Ala Thr Leu Gln Thr Leu Thr Ala Thr Gly Asn Pro Ile Asn Val		
260	265	270
Val Gly Asp His Pro Gln Ala Thr Pro Ala Pro Ala Pro Asp Ala Ser		
275	280	285
Thr Glu Leu Pro Ala Ser Met Ser Gln Ala Gln His Leu Ala Ala Asn		
290	295	300
Thr Ala Thr Asp Asn Tyr Arg Ile Pro Ala Ile Pro Pro Pro Pro Met		
305	310	315
Gly Thr Cys Ser Ser Pro Thr Thr Ser Ala Arg Arg Thr Thr Ala Thr		
325	330	335
Ala Ala Ala Thr Thr Pro Asn Pro Asn His Ile Val Gln Arg Arg Ser		
340	345	350
Thr Asp Gly Gly Lys Thr Trp Ser Ala Pro Thr Tyr Ile His Gln Gly		
355	360	365
Thr Glu Thr Gly Lys Lys Val Gly Tyr Ser Asp Pro Ser Tyr Val Val		
370	375	380
Asp His Gln Thr Gly Thr Ile Phe Asn Phe His Val Lys Ser Tyr Asp		
385	390	395
Gln Gly Trp Gly Gly Ser Arg Gly Gly Thr Asp Pro Glu Asn Arg Gly		
405	410	415
Ile Ile Gln Ala Glu Val Ser Thr Ser Thr Asp Asn Gly Trp Thr Trp		
420	425	430
Thr His Arg Thr Ile Thr Ala Asp Ile Thr Lys Asp Lys Pro Trp Thr		
435	440	445
Ala Arg Phe Ala Ala Ser Gly Gln Gly Ile Gln Ile Gln His Gly Pro		
450	455	460
His Ala Gly Arg Leu Val Gln Gln Tyr Thr Ile Arg Thr Ala Gly Gly		
465	470	475
Pro Val Gln Ala Val Ser Val Tyr Ser Asp Asp His Gly Lys Thr Trp		
485	490	495
Gln Ala Gly Thr Pro Ile Gly Thr Gly Met Asp Glu Asn Lys Val Val		
500	505	510
Glu Leu Ser Asp Gly Ser Leu Met Leu Asn Ser Arg Ala Ser Asp Gly		
515	520	525
Ser Gly Phe Arg Lys Val Ala His Ser Thr Asp Gly Gly Gln Thr Trp		
530	535	540
Ser Glu Pro Val Ser Asp Lys Asn Leu Pro Asp Ser Val Asp Asn Ala		
545	550	555
Gln Ile Ile Arg Ala Phe Pro Asn Ala Ala Pro Asp Asp Pro Arg Ala		
565	570	575
Lys Val Leu Leu Leu Ser His Ser Pro Asn Pro Arg Pro Trp Cys Arg		
580	585	590